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Fig. 1a

GAATTCGCGG CCGCTCTTG CGGTCCAGA GTGGAGTGA AGTCTGGAG CTTTGGGAGG	60
AGACGGGGAG GACAGACTGG AGGCGTGTTC CTCGCGGATT TTCTTTTTCG TGCAGCCCT	120
CGCGCGCGCG TACAGTCATC CCGCTGTCT GACGATTGTG GAGAGGCGGT GGAGAGGCTT	180
CATCCATCCC ACCCGTCTGT CGCGGGGAT TGGGGTCCA GCGACACCTC CCGGGGAGAA	240
GCAGTGCCCA GGAAGTTTTC TGAAGCCGGG GAAGCTGTGC AGCCGAAGCC GCGCCGCGCG	300
CGGAGCCCGG GACACCGGCC ACCCTCCGCG CCACCCACCC TCGCTTTCTC CGGCTTCTC	360
TGGCCGAGGC GCGCGCGGA CCGGCAGCT GTCTGCGCAC GCGAGCTCC ACGGTGAAAA	420
AAAAAGTGAA GGTGTAAAAG CAGCACAAGT GCAATAAGAG ATATTCTCTC AAATTTGCCT	480
CAAG ATG GAA ACC CTT TGC CTC AGG GCA TCC TTT TGG CTG GCA CTG GTT	529
Met Glu Thr Leu Cys Leu Arg Ala Ser Phe Trp Leu Ala Leu Val	
-20 -15 -10	577
GGA TGT GTA ATC AGT GAT AAT CCT GAG AGA TAC AGC ACA AAT CTA AGC	
Gly Cys Val Ile Ser Asp Asn Pro Glu Arg Tyr Ser Thr Asn Leu Ser	
-5 -1 1 5 10	
AAT CAT GTG GAT GAT TTC ACC ACT TTT CGT GGC ACA GAG CTC AGC TTC	625
Asn His Val Asp Asp Phe Thr Thr Phe Arg Gly Thr Glu Leu Ser Phe	
15 20 25	
CTG GTT ACC ACT CAT CAA CCC ACT AAT TTG GTC CTA CCC AGC AAT GGC	673
Leu Val Thr Thr His Gln Pro Thr Asn Leu Val Leu Pro Ser Asn Gly	
30 35 40	
TCA ATG CAC AAC TAT TGC CCA CAG CAG ACT AAA ATT ACT TCA GCT TTC	721
Ser Met His Asn Tyr Cys Pro Gln Gln Thr Lys Ile Thr Ser Ala Phe	
45 50 55	
AAA TAC ATT AAC ACT GTG ATA TCT TGT ACT ATT TTC ATC GTG GGA ATG	769
Lys Tyr Ile Asn Thr Val Ile Ser Cys Thr Ile Phe Ile Val Gly Met	
60 65 70 75	

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Fig. 1b

GTG GGG AAT GCA ACT CTG CTC AGG ATC ATT TAC CAG AAC AAA TGT ATG	817
Val Gly Asn Ala Thr Leu Leu Arg Ile Ile Tyr Gln Asn Lys Cys Met	
80 85 90	
AGG AAT GGC CCC AAC GCG CTG ATA GCC AGT CTT GCC CTT GGA GAC CTT	865
Arg Asn Gly Pro Asn Ala Leu Ile Ala Ser Leu Ala Leu Gly Asp Leu	
95 100 105	
ATC TAT GTG GTC ATT GAT CTC CCT ATC AAT GTA TTT AAG CTG CTG GCT	913
Ile Tyr Val Val Ile Asp Leu Pro Ile Asn Val Phe Lys Leu Leu Ala	
110 115 120	
GGG CGC TGG CCT TTT GAT CAC AAT GAC TTT GGC GTA TTT CTT TGC AAG	961
Cly Arg Trp Pro Phe Asp His Asn Asp Phe Gly Val Phe Leu Cys Lys	
125 130 135	
CTG TTC CCC TTT TTG CAG AAG TCC TCG GTG GGG ATC ACC GTC CTC AAC	1009
Leu Phe Pro Phe Leu Gln Lys Ser Ser Val Gly Ile Thr Val Leu Asn	
140 145 150 155	
CTC TGC GCT CTT AGT GTT GAC AGG TAC AGA GCA GTT GCC TCC TGG AGT	1057
Leu Cys Ala Leu Ser Val Asp Arg Tyr Arg Ala Val Ala Ser Trp Ser	
160 165 170	
CGT GTT CAG GGA ATT GGG ATT CCT TTG GTA ACT GCC ATT GAA ATT GTC	1105
Arg Val Gln Gly Ile Gly Ile Pro Leu Val Thr Ala Ile Glu Ile Val	
175 180 185	
TCC ATC TGG ATC CTG TCC TTT ATC CTG GCC ATT CCT GAA GCG ATT GGC	1153
Ser Ile Trp Ile Leu Ser Phe Ile Leu Ala Ile Pro Glu Ala Ile Gly	
190 195 200	
TTC GTC ATG GTA CCC TTT GAA TAT AGG GGT GAA CAG CAT AAA ACC TGT	1201
Phe Val Met Val Pro Phe Glu Tyr Arg Gly Glu Gln His Lys Thr Cys	
205 210 215	

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Fig. 1c

ATG CTC AAT GCC ACA TCA AAA TTC ATG GAG TTC TAC CAA GAT GTA AAG	1249
Met Leu Asn Ala Thr Ser Lys Phe Met Glu Phe Tyr Gln Asp Val Lys	
220 225 230 235	
GAC TGG TGG CTC TTC GGG TTC TAT TTC TGT ATG CCC TTG GTG TGC ACT	1297
Asp Trp Trp Leu Phe Gly Phe Tyr Phe Cys Met Pro Leu Val Cys Thr	
240 245 250	
GCG ATC TTC TAC ACC CTC ATG ACT TGT GAG ATG TTG AAC AGA AGG AAT	1345
Ala Ile Phe Tyr Thr Leu Met Thr Cys Glu Met Leu Asn Arg Arg Asn	
225 260 265	
GGC AGC TTG AGA ATT GCC CTC AGT GAA CAT CTT AAG CAG CGT CGA GAA	1393
Gly Ser Leu Arg Ile Ala Leu Ser Glu His Leu Lys Gln Arg Arg Glu	
270 275 280	
GTG GCA AAA ACA GTT TTC TGC TTG GTT GTA ATT TTT GCT CTT TGC TGG	1441
Val Ala Lys Thr Val Phe Cys Leu Val Val Ile Phe Ala Leu Cys Trp	
285 290 295	
TTC CCT CTT CAC TTA AGC CGT ATA TTG AAG AAA ACT GTG TAT AAC GAA	1489
Phe Pro Leu His Leu Ser Arg Ile Leu Lys Lys Thr Val Tyr Asp Glu	
300 305 310 315	
ATG GAC AAG AAC CGA TGT GAA TTA CTT AGT TTC TTA CTG CTC ATG GAT	1537
Met Asp Lys Asn Arg Cys Glu Leu Leu Ser Phe Leu Leu Leu Met Asp	
320 325 330	
TAC ATC GGT ATT AAC TTG GCA ACC ATG AAT TCA TGT ATA AAC CCC ATA	1585
Tyr Ile Gyr Ile Asn Leu Ala Thr Met Asn Ser Cys Lile Asn Pro Ile	
335 340 345	
GCT CTG TAT TTT GTG AGC AAG AAA TTT AAA AAT TGT TTC CAG TCA TGC	1633
Ala Leu Tyr Phe Val Ser Lys Lys Phe Lys Asn Cys Phe Gln Ser Cys	
350 355 360	

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Fig. 1d

CTC	TGC	TGC	TGC	TGT	TAC	CAG	TCC	AAA	AGT	CTG	ATG	ACC	TGG	GTC	CCC	1681
Leu	Cys	Cys	Cys	Cys	Tyr	Gln	Ser	Lys	Ser	Leu	Met	Thr	Ser	Val	Pro	
365			370			375										
ATG	AAC	GGA	ACA	AGC	ATC	CAG	TGG	AAG	AAC	CAC	GAT	CAA	AAC	AAC	CAC	1729
Met	Asn	Gly	Thr	Ser	Ile	Gln	Trp	Lys	Asn	His	Asp	Gln	Asn	Asn	His	
380			385			390			395							
AAC	ACA	GAC	CGG	AGC	AGC	CAT	AAG	GAC	AGC	ATG	AAC	TGACCACCCT	1775			
Asn	Thr	Asp	Arg	Ser	Ser	His	Lys	Asp	Ser	Met	Asn					
400			405													
TAGAAGCACT	CCTCGGTACT	CCCATAATCC	TCTCGGAGAA	AAAAATCACA	AGGCAACTGT	1835										
GACTCCGGGA	ATCTCTTCTC	TGATCCTTCT	TCCTTAATTC	ACTCCACAC	CCAAGAAGAA	1895										
ATGCTTTCCA	AAACCGCAAG	GTAGACTGGT	TTATCCACCC	ACAACATCTA	CGAATCGTAC	1955										
TTCTTTAATT	GATCTAA	TTACATATTCTG	CGTGTGTAT	TCAGCACTAA	AAAATGGTGG	2015										
GAGCTGGGGG	AGAATGAAGA	CTGTAAATG	AAACCAGAAG	GATTTTACT	ACTTTTGCAT	2075										
GAAAAATAGAG	CTTTCAAGTA	CATGGCTAGC	TTTTATGGCA	GTTCTGGTGA	ATGTTCAATG	2135										
GGAACTGGTC	ACCATGAAAC	TTTAGAGATT	AACGACAAGA	TTTTCTACTT	TTTTTAAGTG	2195										
ATTTTTTGTG	CTTCAGGCCAA	ACACAATATG	GGCTCAGGCT	ACTTTTATTT	GAAATGTGAT	2255										
TTGGTGCCAG	TATTTTTTAA	CTGCATAATA	GCCTAACATG	ATTATTGGAA	CTTATTTACA	2315										
CATAGTTTGA	AAAAAAAAAG	ACAAAAATAG	TATTCAGGTG	AGCAATTAGA	TTAGTATTTT	2375										
CCACGTCACT	ATTATTTTTT	TTAAAAACAC	AATTCTAAAG	CTACAACAAA	TACTACAGGC	2435										
CCTTAAAGCA	CAGTCTGATG	ACACATTTGG	CAGTTTAATA	GATGTTACTC	AAAGAATTTT	2495										
TTAAGAAGCTG	TATTTTATTT	TTTAAATGGT	GTTTTATTAC	AGGGGACCTT	GAACATGTTT	2555										
TGTATGTTAA	ATTCAAAAGT	AATGCTTCAA	TCAGATAGTT	CTTTTTCACA	AGTTCAATAC	2615										
TGTTTTTCAT	GTAATTTTTG	TATGAAAAAT	CAATGTCAAG	TACCAAAATG	TTAATGTATG	2675										
TGTCATTTAA	CTCTGCCTGA	GACTTTCAGT	GCACTGTATA	TAGAAGTCTA	AAACACACCT	2735										
AAGAGAAAAA	GATCGAATTT	TTCAGATGAT	TGGGAAATTT	TCAATTCAGGT	ATTGTGAATA	2795										

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Fig. 1e

GTGACATATA TATGTATATA CATATCACCT CCTATTCTCT TAATTTTGT TAAATGTTA	2855
ACTGGCAGTA AGTCTTTTTT GATCATTCCC TTTTCCATAT AGGAAACATA ATTTGAAGT	2915
GGCCAGATGA GTTTATCATG TCAGTGAAAA ATAATTACCC ACAATGCCA CCAGTAACCT	2975
AAGGATTCTT CACTTCTTGG GGTTTTCTAGT ATGAACCTAA CTCCCCACCC CAACATCTCC	3035
CTCCACATT GTCAACATTT CAAAGGGCCC ACAGTGACTT TTGCTGGCCA TTTTCCAGA	3095
TGTTTACAGA CTGTGAGTAC AGCAGAAAAAT CTTTACTAC TGTGTGTGTG TATATATATA	3155
AACAATTGTA AATTTCITTT AGCCCATTTT TCTAGACTGT CTCTGTGGAA TATATTTGTG	3215
TGTGTGATAT ATGCATGTGT GTGATGGTAT GTATGGA <u>TTT</u> AATCTAATCT AATAATTGTG	3275
CCCCGCAGTT GTGCCAAAGT GCATAGTCTG AGCTAAAATC TAGGTGATTG TTCATCATGA	3335
CACCCGCGCT CAGTCCATTT TAACCTGTAG CAACCTTCTG CATTCTATAA TCTTGAATC	3395
ATGTTACCAT TACAAATGGG ATATAAGAGG CAGCGTGAAA GCAGATGAGC TGTGGACTAG	3455
CAATATAGGG TTTTGTITGG TTGTTGGTT TGATAAGCA GTATTTGGGG TCATATTGTT	3515
TCCTGTCTG GAGCAAAAGT CATTACACTT TGAAGTATTA TATTGTTCTT ATCCTCAATT	3575
CAATGTGGTG ATGAAATTGC CAGGTGTCT GATATTTCTT TCAGACTTCG CCAGACAGAT	3635
TGCTGATAAT AAATTAGGTA AGATAATTG TTGGGCCATA TTTTAGGACA GGTAAAAATA	3695
CATCAGGTTG CAGTGTCTG AATTGCAAGG CTAAGAAGTA CTGCCCTTTT GTGTGTTAGC	3755
AGTCAAATCT ATTATTCCAC TGGCGCATCA TATGCACTGA TATATGCTTA TAATATAAGC	3815
CATAGGTTCA CACCATTTTG TTTAGACAAT TGTCTTTTT TCAAGATGCT TTGTTTCTTT	3875
CATATGAAAA AAATGCATTT TATAAATTCA GAAAGTCATA GATTTCGTAA GCGTCAACG	3935
TGCATTTTAT <u>TTAT</u> GGACTG GTAAGTAACT GTGGTTTACT AGCAGGAATA TTTCCAATTT	3995
CTACCTTTAC TACATCTTTT CAACAAGTAA CTTTGTAGAA ATGAGCCAGA AGCCAAGGCC	4055
CTGAGTTGGC AGTGGCCCAT AAGTGTA <u>AAA</u> <u>TAAA</u> AGTTTA CAGAAACCTT	4105

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Fig. 2a

GAGACATTCC GGTGGGGGAC TCTGGCCAGC CCGAGCAAACG TGGATCCTGA GAGCACTCCC	60
AGGTAGGCAT TTGCCCCGGT GGGACGCCTT GCCAGACCAG TGTGTGGCAG GCCCCCGTGG	120
AGGATCAACA CAGTGCCTGA ACACTGGGAA GGAACCTGTA CTTGGAGTCT GGACATCTGA	180
AACCTGGCTC TGAACTGCG GAGCGGCCAC CGGACGCCTT CTGGAGCAGG TACGAGC	237
ATG CAG CCG CCT CCA AGT CTG TGC GGA CGC GCC CTG GTT GCG CTG GTT	285
Met Gln Pro Pro Pro Ser Leu Cys Gly Arg Ala Leu Val Ala Leu Val	
1 5 10 15	
CTT GCC TGC GGC CTG TCG CGG ATC TGG GGA GAG GAG AGA GGC TTC CCG	333
Leu Ala Cys Gly Leu Ser Arg Ile Trp Gly Glu Glu Arg Gly Phe Pro	
20 25 30	
CCT GAC AGG GCC ACT CCG CTT TTG CAA ACC GCA GAG ATA ATG ACG CCA	381
Pro Asp Arg Ala Thr Pro Leu Leu Gln Thr Ala Glu Ile Met Thr Pro	
35 40 45	
CCC ACT AAG ACC TTA TGG CCC AAG GGT TCC AAC GCC AGT CTG GCG CGG	429
Pro Thr Lys Thr Leu Trp Pro Lys Gly Ser Asn Ala Ser Leu Ala Arg	
50 55 60	
TCG TTG GCA CCT GCG GAG GTG CCT AAA GGA GAC AGG ACG GCA GGA TCT	477
Ser Leu Ala Pro Ala Glu Val Pro Lys Gly Asp Arg Thr Ala Gly Ser	
65 70 75 80	
CCG CCA CGC ACC ATC TCC CCT CCC CCG TGC CAA GGA CCC ATC GAG ATC	525
Pro Pro Arg Thr Ile Ser Pro Pro Pro Cys Gln Gly Pro Ile Glu Ile	
85 90 95	
AAG GAG ACT TTC AAA TAC ATC AAC ACG CTT GTG TCC TGC CTT GTG TTC	573
Lys Glu Thr Phe Lys Tyr Ile Asn Thr Val Val Ser Cys Leu Val Phe	
100 105 110	

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Fig. 2b

GTG CTG GGG ATC ATC GGG AAC TCC ACA CTT CTG AGA ATT ATC TAC AAG	621
Val Leu Gly Ile Ile Gly Asn Ser Thr Leu Leu Arg Ile Ile Tyr Lrs	
115 120 125	
AAC AAG TGC ATG CGA AAC GGT CCC AAT ATC TTG ATC GCC AGC TTG GCT	669
Asn Lys Gys Met Arg Asn Gly Pro Asn Ile Leu Ile Ala Ser Leu Ala	
130 135 140	
CTG GGA GAC CTG CTG CAC ATC GTC ATT GAC ATC CCT ATC AAT GTC TAC	717
Leu Gly Asp Leu Leu His Ile Val Ile Asp Ile Pro Ile Asn Val Tyr	
145 150 155 160	
AAG CTG CTG GCA GAG GAC TGG CCA TTT GGA GCT GAG ATG TGT AAG CTG	765
Lys Leu Leu Ala Glu Asp Trp Pro Phe Gly Ala Glu Met Cys Lys Leu	
165 170 175	
GTG CCT TTC ATA CAG AAA GCC TCC GTG GGA ATC ACT GTG CTG AGT CTA	813
Val Pro Phe Ile Gln Lys Ala Ser Val Gly Ile Thr Val Leu Ser Leu	
180 185 190	
TGT GCT CTG AGT ATT GAC AGA TAT CGA GCT GTT GCT TCT TGG AGT AGA	861
Cys Ala Leu Ser Ile Asp Arg Tyr Arg Ala Val Ala Ser Trp Ser Arg	
195 200 205	
ATT AAA GGA ATT GGG GTT CCA AAA TGG ACA GCA GTA GAA ATT GTT TTG	909
Ile Lys Gly Ile Gly Val Pro Lys Trp Thr Ala Val Glu Ile Val Leu	
210 215 220	
ATT TGG GTG GTC TCT GTG GTT CTG GCT GTC CCT GAA GCC ATA GGT TTT	957
Ile Trp Val Val Ser Val Val Leu Ala Val Pro Glu Ala Ile Gly Phe	
225 230 235 240	
GAT ATA ATT ACG ATG GAC TAC AAA GGA AGT TAT CTG CGA ATC TGC TTG	1005
Asp Ile Ile Thr Met Asp Tyr Lys Gly Ser Tyr Leu Arg Ile Cys Leu	
245 250 255	

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Fig. 2c

CTT CAT CCC GTT CAG AAG ACA GCT TTC ATG CAG TTT TAC AAG ACA GCA	1053
Leu His Pro Val Gln Lys Thr Ala Phe Met Gln Phe Tyr Lys Thr <u>Ala</u>	
260 265 270	
AAA GAT TGG TGG CTG TTC AGT TTC TAT <u>TTC</u> TGC TTG CCA TTG GCC ATC	1101
Lys Asp Tyr Trp Leu Phe Ser Phe Tyr Phe Cys Leu Pro Leu Ala Ile	
275 280 285	
ACT GCA TTT TTT TAT ACA CTA ATG ACC TGT GAA ATG TTG AGA AAG AAA	1149
Thr Ala Phe Phe Tyr Thr Leu Met Thr Cys Glu Met Leu Arg Lys Lys	
290 295 300	
AGT GCC ATG CAG ATT GCT TTA AAT GAT CAC CTA AAG CAG AGA CGG GAA	1197
Ser Gly Met Gln Ile Ala Leu Asn Asp His Leu Lys Gln Arg Arg Glu	
305 310 315 320	
GTG GCC AAA ACC GTC TTT TGC CTG GTC CTT GTC TTT GCC CTC TGC TGG	1245
Val Ala Lys Thr Val Phe Cys Leu Val Leu Val Phe Ala Leu Cys Trp	
325 330 335	
CTT CCC CTT CAC <u>CTC</u> AGC AGG ATT CTG AAG CTC ACT GTT TAT AAT CAG	1293
Leu Pro Leu His Leu Ser Arg Ile Leu Lys Leu Thr Leu Tyr Asp Gln	
340 345 350	
AAT GAT CCC AAT AGA TGT GAA CTT TTG AGC TTT CTG TTG GTA TTG GAC	1341
Asn Asp Pro Asn Arg Cys Glu Leu Leu Ser Phe Leu Leu Val Leu Asp	
355 360 365	
TAT ATT GGT ATG AAC <u>ATG</u> GCT TCA CTG AAT TCC TGC ATT AAC CCA ATT	1389
Tyr Ile Gyr Ile Asn Met Ala Ser Leu Asn Ser Cys Ile Asn Pro Ile	
370 375 380	
GCT CTG TAT TTC GTG AGC AAA AGA TTC AAA AAC TGC TTT AAG TCA TGC	1437
Ala Leu Tyr Leu Val Ser Lys Arg Phe Lys Asn Cys Phe Lys Ser Cys	
385 390 395 400	

Fig. 2d

TTA TGC TGC TGG TGC CAG TCA TTT GAA GAA AAA CAG TCC TTG GAG GAA	1485
Leu Cys Cys Trp Cys Gln Ser Phe Glu Glu Lys Gln <u>Ser</u> Leu Glu Glu	
405 410 415	
AAG CAG TCG TGC TTA AAG TTC AAA GCT AAT GAT CAC GGA TAT GAC AAC	1533
Lys Gln <u>Ser</u> Cys Leu Lys Phe Lys Ala Asn Asp His Gly Tyr Asp Asn	
420 425 430	
TTC CGT TCC AGT AAT AAA TAC AGC TCA TCT TGAAAGAAGA ACTATTTCACT	1583
Phe Arg <u>Ser</u> <u>Ser</u> Asn Lys Tyr <u>Ser</u> Ser Ser	
435 440	
GTATTTTCATT TTCCTTTATAT TGGACCGAAG TCATTAAAAAC AAAATGAAAC ATTTGCCAAA	1643
ACAAAAACAAA AAACATGTGA TTTGCACAGC ACACT <u>ATTAA</u> AATATTAAGT GTAATTATTT	1703
TAACTACT <u>CAC</u> AGCTACATAT GACATTTTAT GAGCTGTTTA CGGCATGGAA AGAAATCAG	1763
AGGGAATTAA GAAAGCCTCG TCGTGAAGAC ACTTAATTTT TTACAGTTAG CACTTCAACA	1823
TAGCTCTTAA CAACTTCCAG GATATTCACA CAACACTTAG GCTTAAAAAT GAGCTCACTC	1883
AGAATTTCTA TTCCTTTCTAA AAAGAG <u>AITTT</u> ATTTTAAAT CAATGGGACT CTGATATAAA	1943
GGAAGAATAA GTCAGTGTAA AACAGAAGTT TTAATGAAG CTAAATTAC TCA <u>AITTTAA</u>	2003
ATTTTAAAAA CCTTTAAAAA AACTTTTCAA TTAATATTAT CACACTATTA TCAGATTGTA	2063
ATTAGATGCA AATGAGAGAG CAGTTTAGTT GTTGCAATTT TCGCACACTG GAAAG <u>ATTTA</u>	2123
AATGATCAGG AGGGAGTAAC AGAAAGAGCA AGGCTGTITT TGAAATTCAT TACACTTTCA	2183
CTAGAAGCCC AAACCTCAGC ATTCTGCAAT ATGTAACCAA CATGTCACAA ACAAGCAGCA	2243
TGTAACAGAC TGGCACATGT GCCAGCTGAA <u>TTTAA</u> AATAT AATACTTTTA AAAAGAAAAAT	2303
TATTACATCC TTTACATTCA GTTAAGATCA AACCTCACAA AGAGAAATAG AATGTTTGAA	2363
AGGCTATCCC AAAAGACTTT TTTGAATCTG TCATTACAT ACCCTGTGAA GACAATACTA	2423
TCTACAATTT TTTCAGGATT ATTAATAATCT TCTTTTTTCA CTATCGTAGC TTAACCTCTG	2483
TTTGGTTTTG TCATCTGTAA ATACTTACCT ACATACACTG CATGTAGATG ATTAATAGAG	2543
GGCAGGCCCT GTGCTCATAG CTTTACGATG GAGAGATGCC AGTGACCTCA <u>TAATAAGAC</u>	2603
TGTGAACATGC CTGGTCAGT GTCCACATGA CAAAGGGGCA GGTAGCACCC TCCTTCACCC	2663

Fig. 2e

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ATGCTGTGGT TAAATGGTT TCTAGCATAT GTATAATGCT ATAGTAAAA TACTATTTT	2723
CAAAATCATA CAGATTAGTA <u>CATT</u> TAAACAG CTACCTGTAA AGCTTATTAC TAATTTTGT	2783
ATTATTTTGT TAAATAGCCA ATAGAAAAGT TTGCTTGACA TGGTGCTTTT CTTCATCTA	2843
GAGGCAAAAC TGCTTTTGA GACCGTAAGA ACCTCTTAGC TTTGTGCGTT CCTGCCTAAT	2903
TTTTATATCT TCTAAGCAAA GTGCCTTAGG ATAGCTTGGG ATGAGATGTG TGTGAAAGTA	2963
TGTACAAGAG AAAACGGAAG AGAGAGGAAA TGAGGTGGGG TTGGAGGAAA CCCATGGGGA	3023
CAGATTCCCA TTCTTAGCCT AACGTTGCTC ATTGCCTCGT CACATCAATG CAAAAGTGCC	3083
TGATTTTGTT CCAGCAAAAC ACAGTGAAT GTTCTCAGAG TGACTTTTGA <u>AATAA</u> ATTGG	3143
GCCCAAGAGC TTTAACTCGG TCTTAAATA TGCCCAAAAT TTTACTTTGT TTTTCTTTTA	3203
ATAGGCTGGG CCACATGTTG GAAATAAGCT AGTAATGTTG TTTTCTGTCA ATATTGAATG	3263
TGATGTTACA GTAAACCAAA ACCCAACAAT GTGGCCAGAA AGAAAGAGCA ATAATAATTA	3323
ATTCACACAC CATATGGATT <u>CTATTT</u> TAA ATCAACCACA AACTTGTTCT TTAATTTCAT	3383
CCCAATCACT TTTTCAGAGG CCTGTTATCA TAGAAGTCAT TTTAGACTCT CAATTTTAAA	3443
TTAATTTTGA ATCACTAATA TTTTCACAGT TTATTAATAT <u>ATTTA</u> ATTTC <u>TATTTA</u> AATT	3503
TTAGATTATT TTTATTACCA TGTAAGTAAT TTTTACATCC TGATACCCCT TCCTCTCCA	3563
TGTCAGTATC ATGTTCTCTA ATTATCTTGC CAAATTTTGA AACTACACAC AAAAAGCATA	3623
CTTGCAATAT <u>TTATAATAAA</u> ATTGCATTCA GTGGCTTTT AAAAAAAAATG TTTGATTCAA	3683
AACTTTAACA TACTGATAAG TAAGAAACAA TTATAATTTT TTTACATACT CAAAACCAAG	3743
ATAGAAAAAG GTGCTATCGT TCAACTTCAA AACATGTTTC CTAGTATTAA GGACTTTAAT	3803
ATAGCAACAG ACAAATTTAT TGTTAACATG GATGTTACAG CTCAAAAGAT <u>TTATA</u> AAAGA	3863
TTTAAACCTA TTTTCTCCCT TATTATCCAC TGCTAATGTG GATGTATGTT CAAACACCTT	3923
TTAGTATTGA TAGCTTACAT ATGCCCAAAG GAATACAGTT TATAGCAAAA CATGGGTATG	3983
CTGTAGCTAA CTTTATAAAA GTGTAATATA ACAATGTAAA AAATTATATA TCTGGGAGGA	4043
TTTTTTGGTT GCCTAAAGTG GCTATAGTTA CTGATTTTTT ATTATGTAAG CAAAACCAAT	4103
<u>AAAAATTTTA</u> GTTTTTTTAA CAACTACCTT ATTTTTCAC GTACAGACAC TAATTCATTA	4163
AATACTAATT GATTGTTTAA AAGAAATATA AATGTGACAA GTGGACATTA <u>TTAT</u> GTTAA	4223
ATATACAATT ATCAAGCAAG TATGAAGTTA TTCAATTA <u>AAA</u> ATGCCACATT TCTGGTCTCT	4283
GGGAAAAAAA AAAAAAAA	4301

105150-2516650

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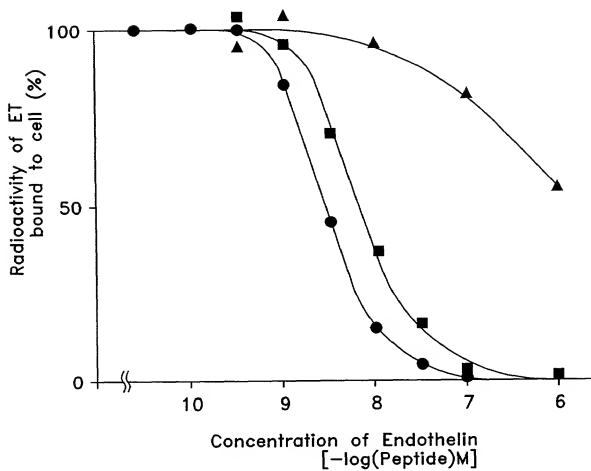


Fig. 3

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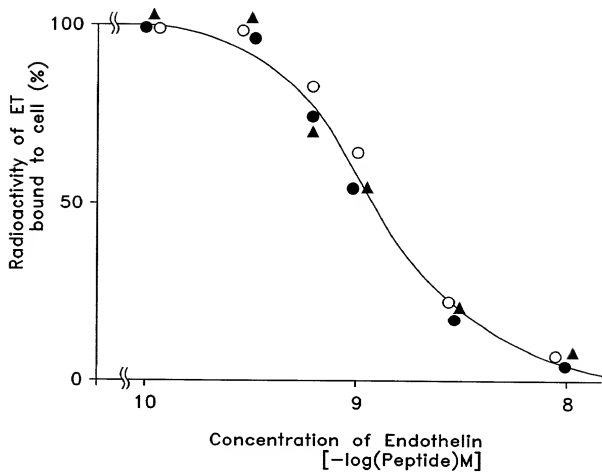


Fig. 4

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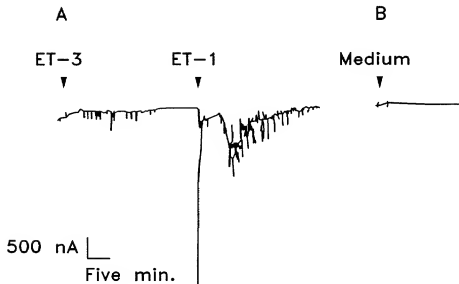
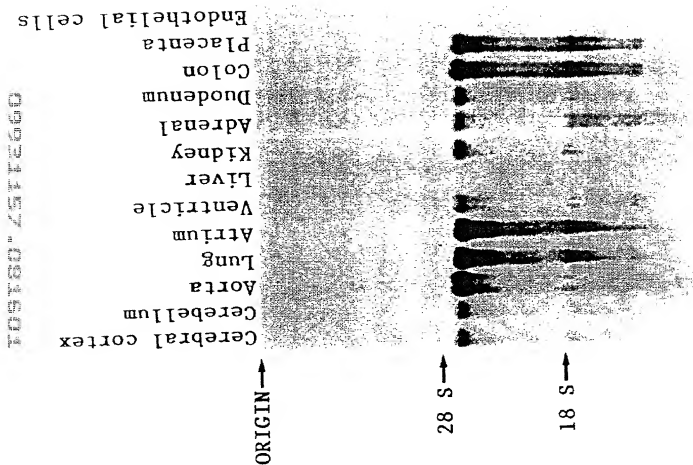


Fig. 5

Fig. 6



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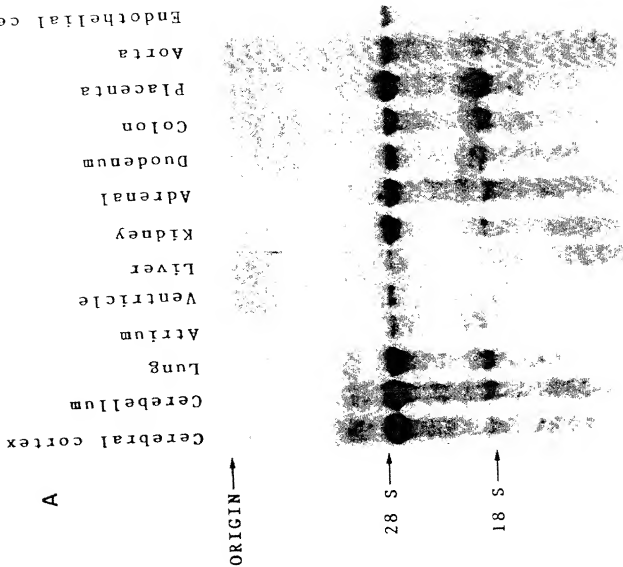


Fig. 7

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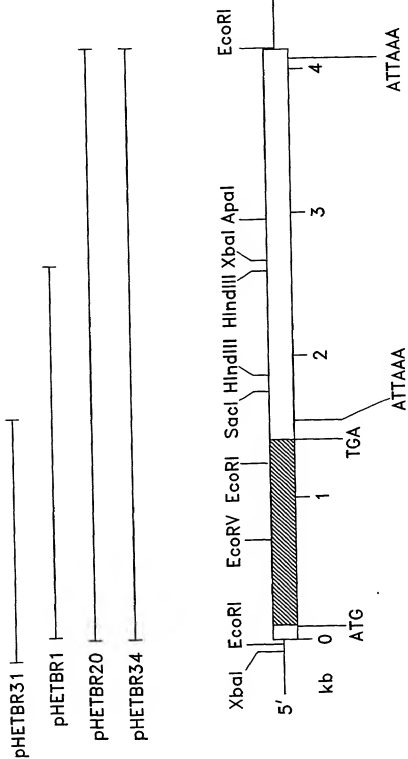


Fig. 8